```
.soform 1:
    I TISCICACIS CICLOSCASS TOST CICCO ATSAGEDASS IN SEGGIST
   SI COTOTTCCTT CT-1-3GSTCC TGGGGGCCCT CACTGLSAIG TGTGAAATAC
  101 CAGAGATGGA CAGCCATCTG GTAJAGAACT TUGGCCAGCA COTCTTACCT
  151 TGGATGGACC GECTTECCT GGACCACTIG AACCCCAGCA TCTATGTGGG
  201 COTACGOOTO TOOPSTOTEGO AGGOTGGOAC CAAGGAAGAC
  $51 ACAGCCTCAA GCTTGGTTAC
                             CASCAGTETC
                                        TCCTLCGGTC TGCCTTCAGC
  301 GAGGATGACG GUGACTGCCA DGGCARGCIT TCCATUGGCC AGCTCGCCCT
  351 CTACCIGCIC GCICICAGAG CCAACIGIDA GIITUTCAGG GGCCACAAGG
  401 GGGACAGGCT GGTCTCACAG
                            CTCAAATOBT POCTGGACGA TGAGAAGAGA
      GCCATTGACA CAGCAGCCAT GGCAGGCIIG GCATTCACCT GTCTGAAGCG
      STOAMASTIC AACCOTGGTO GGAGASAASG GAICASCAIG GCCATCAGAA
  551 CAGTECBAGA GGAGATOTTG AABGCCCABA COCCCBAGGG CCACTTTGGG
  601 AAIGTOTADA GCACCCCATT GGCALLACAG ITOOTOALGA CTTCCCCCDAT
     GCGTGGGGCA GAACTGGGAA
                            CARCAIDIDE CAARRIGAGE GTTGCTTIGC
  701 PÁBOCCABICI GCAGGATGGA BOCTLOCCAG ATBOLCTCAT GATTTCCCAG
      OTECTEDOS TROTGAACCA CAAGACCIAC ATREATOTGA TOTTCOCAGA
      CIGICIGGCA
                 CDACGAGTDA FETTEGRADO AGORGOTGAS ACCATRODES
  BB1 AGACCCAAGA GAICATCAGT GICACGCTGC AGGTGCTTAG TOTOTIGCCG
  301 COGTACAGAD AGROCATOTO TGRTCLEGOD
                                        BG BTC CACCG
  351
     COTGAAGAAG GOCCATGAGG TAGGAGGATG
                                        CACATATGAA ACACAGGCOT
 1001 CONTGREAGE
                 COCCIACTTA ACCIDECTEA TGESSAAAGC
 1051 AGGGAGTTOT GGGAGCTTOT COGAGACOCC AACACCOCAC TGTTGCAAGG
1101 TATTGOTEAC TACABACCOA AGBATEBABA AADDATTBAG OTGABGOTGG
1951 TTAGOT GOTA FOCCOTGAGO TO COCOATO CHAGOAGOTO GOACACTOCO
 1:01 TAGGOTIOTA COCTOCCTIC TGATGTICIT GGAACAGGAA DICGOCTGAC
1151 COTECT FOCA COTCOTGT FO ACTIFIEDS IN ATSUDUCTION FIGATOACCCC
1001 AGCCACAAGC
                 COTTOGAG GO COCTATAC NA TELECOT
1551 AGCOAN ICAT CUTCOCTGGG MARTICTT IT GGGGAASTOT
                                                   GGCCAGCCTG
1401 GOODG AGG TOTCCCATGA AGGCCACOUC ATGUR MGAT GGGCATGAAG
1451 CATCTCLGAC
                ICCTTGGCAA AAAACEGA TI CCGCACECCG CAGGTGTTGT
1501 GAAGACCACT
                 IGTTCTGTGG TTGGG TTDCT GCZVGWAGGC CTCCTCAGCC
1551 CEGGGGGTAT
                 GGCCCTGACC CCAGCFCTOC ACTOTOCOTGT TAGAGTGGCA
1601 Geterowaert
                 FETTGTGGCA CACTAGCIGG GGAGACCICA GCAGGGCTGC
1631 TCAGTCCCIG COTCTGACAA FATTAAAGCA TTGATCGCCT GTGAAAAAAA
1701 AMARAGAMA AAAAAAAAAA FA
(SEC ID NO:1
```

# FEATURES:

5'UTR: 1 - 3 Start Codor: 31 Stop Codon: 1159 3'UTF: 1162

## Homologous proteins:

Top 10 ELAST Fits

37.21.20.20.00.45	Score	E
<pre>CHA  108000024553390 'altid=gi  127427' def=ref XI 009322.2  tr</pre>	752	0.0
CEA 108000024635236	732	0.0
- UFA[18000004925123 /altid=gi 339205	732	0.0
-CFA 108000024043636	731	0.0
CFA(18000004926130 /altid=qi(45074)9 /def=tef(MP (50)345. tran	727	0.0
CFAT18000004926132 /altid=qi[3392]; /qef=qb[AAA61656.1	725	
CFATIE000005170902 /altid=qi 7657639 .def=gef NP (55364.   tran	5, 1 5	e-145
CFA 18000005218941 /altid-gi 457:454 /def=jb AAD23323.1/AF12128	501	
CFA  64000136745249 ,altid=gi; 11)68124 ,de:=ref MF 071979.1  tr	401	
CRA 18000004926154 /altid=qi 4507407 /def=ref NP_001053.1  tran	401	e-134
do	108	26-22

#### EXPRESSION INFORMATION FOR MODULATORY USE:

library source:

gi|10725490|adult adrenal gland
gi|10947399| mammary gland
gi|9121397| retinoblastoma
gi|13230819| adenocarcinoma cell line
gi|13237907| retinoblastoma
gi|13216505| embryonal carcinoma, cell line
gi|8150776| adult uterus
gi|5936410| adult uterus
gi|6858875| adult head\_neck
gi|6858872| adult head\_neck

<u>Tissue Expression:</u> Human leukocyte

Ish: En 2: I COAGGATIAA TEAGTGACAS SAAGETTOST CTCTCGGAGG GGTGACDAGG 51 TOTGOT BASE ASAGCCTCAG CAGGGCCAGO CCCAGGAGTC TTTCCCGATT 101 CTTGCTCACT GCTCACCCAC CTCCTGCTGC CATGAGGCAC CTTGGGGCCT 151 TOCTOTTOGT TOTGGGGGGTO CTCGGGGGCCO TCACTGAGAT GTGTGAAATA 201 CCAGAGATGG ACAGCCATCT GGT&CAGAAG TTGGGCCAGC ACCTCTTACC 2 1 TTCGATGGAC OGGETTTECC TGCACCACTT GAACCCCAGC ATCTATGTGS GCCTACCCCT STCCAGTCTG CASCCTGUGA CCAAGGAAGA CCICTACCIG 1.1 CACAGCOTCA IGCTTGGTTA CCACCAGTGC CTCCTACGGT CTCCCTTCAG H 1 CGAGGATCAC GTGACTGCC AGGCCAAGCC TTCCATCGGC CAGCTGGCCC 1.1 TOTACCTO IT COCTOTOAGA GOCAACTGGC ATGATCADAA DGGCCACCCC 161 CACACTAC T ACTACCACTA IGGCOTOGGO ATTOTGDCCC IGGGTCTCCA 11 CCABALGC IG STCCATGACA SCGTGGTGGA CARACTICTS TARBUTGTGG · C1 AACCITIC A CCAGGGCCAC CATICTGIGG ACACAGCACC CATEGOAGGO #81 TTESCAPT A CCTSTCTGAA SCGCTCAAAC TTCAACCCTS STCSEAGACA OF ACTESATION OF ATGROCCATION RANDAGTIGGS AGAINGNATIO - TIPGAA GGCCC 191 AUA 2000CHA GGGCCACTIT GGRAAPGICT ADADOADOOD AITGGDATTA CGACTTCCCC CALGOTTGGG GCALAACTGG GAACAGCATG -(1 CARRICCI A -51 COLUMAGGIG AGGGITGOTT TGCTGGCCAG TOTGCASSAI C1 ABARTOST T 'ATGAITTCC CABUIGOIGO COGIICIBAA OCACAAGACO #1 TADATTGATO TSATORTOCO AGADIGTOTS GOADCAUGAS TOADGOTSGA 1:11 ACMARTOT BAGACCATTO OTCAGACCOA AGAGACCATO AGTGICACGO 1 81 TECAMETER T MAGNETETTS MESCESTAGA GACAGICMAT CHARBUTTERS 1101 GOODGETC A ICGTGGAAGA COTOCTGAAG AAG COCATO AGITAGGAGG 1131 APT ACATAT PANACACAGO COTOCTTOTO AGGICOCTAC TRANCOTOCG 1.01 TOATGOOGA AGCGGCCGGA HAAAGGGAGT TOT GCANCT TOTOLDAGAC COMADÃO O HACTOTEGOA AGGUATEGOT GAGUACAGAO COMA BIATGO 1.51 1:01 A NAVANDATT MAGCTGAGGC JOGGTTAQCTG GTA-CCOLF AGTTHCCTCA 1:51 I KUTA 30A 30 TOGGACACT HOOMAGGOTT ONAFIDOTION TO THUATERO DITHUAACAG HAACTCGCCT 1101WACCOLEGIG COMOSTOURS TELL TITGA 1:513 34.79.70 10 TGGGATCAC CCAGCCACA AGCCOTTOGA GIRCOCTATA P. DOED FY: C GTTGGAGCA AGAGDDAAG CATHITICCON BUBLAGTOIT 1 51 TOURNALS TOUGGOCAGO HTGRODOTGC AGGIDTOCCA TGAAGGOCAC DICATIBET " HATGGGCATG AAGCAICTCA GACTICITGI CAAAAAACGG 1.51 A H (COCA); COGCAGGTGT CGTCAAGACC ACTUGTTCTG TGGTTCGGGGT FE CHICHAGAA GECTECTEA GECEGGGGG TATUGCTETG ACCICAGCTE TOTATIÓTOS ISTTAGAGTG GCACCTCCGA GCTUGTICTO GCATACTAGC THEGELAGACO CHAGCAGGGC NGCHCAGTGC CTGCCTCTGA CAAAASTAAA 1831 GCASTONTOR CITGTGAAAA LAARAAAAA AAAAAAAAAA AAAAAAAA (SEQ ID NO:

#### FEATURES:

5'UTA: 1 - 131 Start C don: 13 Stop Compa: 13-2

3'UTF: 13 5

#### Homologous proteins:

Top 10 FLA31 Hi's

0721212	Score	E
CRA 1080 (0).4536.46 altid=gi 293316 /def=gb AAF:5526.1 trans	793	0.0
CEA  1080  3) 34553130   altid=qi  1274  175   /daf=ref  /P 0594555 /	702	0.0
CRA(IROUCD): #2517 / altid=qi[339200 /def=qb]AAAA205 / 1,	700	0.0
-CEA:13800JJ::420:6	790	0.0
_ChA I.UUUU)::::::::// / iltid=gi 43074(@//def=ref NP-00u34,   1  + cap	700	0.0
CFA 130000019:51:://iltid=gi 339201/def=gb AAA&1056.1/(L02647	786	0.0
CFA(1800000) 1'09(2 / iltid=qi 76576)9 /def=ref(NP 05656: 1) tran	561	e-159
CEA 164000156/45249 /altid=gi 11968124 /def=ref NP_071979.1  tr	554	e-156

CRA(180 0005.1894) Zairid adil4522454 Zdors gotavicka, c.1(AF121za CRA(180000049zči34 zairid-dil4507407 Zdor sef.55 + 1053.1) tran	545 128	α = 1 0 .4 1 α = ±1 ≤
EST:		
qii10 25490 /dataset=dbest /taxon=96	853	0.0
gi 5936410 /dataset=dbest /taxon=9606	835	0.0
gi 68d8P75 /dataset=dbest /tamon=9606	726	0.5
gil68/8872 /dataset=dbest /taxon=9606	726	0.0
gi 12258937		0.0
gif10447399 /dataset=dbest /taxon=96	680	0.0
gi 13287907 /dataset=dbest /taxon=96	680	0.0
gi 9:21897 /dataset=dbest /taxon=9606	680	0.0
gil11280319 /dataset=dbest /taxon=96	680	0.0
gi[8]50776 /dataset=dbest /taxon=960	656	0.0

# EXPRESSION INFORMATION FOR MODULATORY USE:

```
library source:
gi[10]:25490| adult adrenal gland
gi[5936410: adult uterus
gi[684-375: adult head_neck
gi[684-372: adult head_neck
gi[122]:3987| adult lung_tumor
gi[109:7339| mammary gland
gi[1328:7907] retinoblastoma
gi[9121897] retinoblastoma
gi[1328:0819] adenocarcinoma cell line
gi[8130776]
```

Tissue Expression: Human hippocampus

```
I MEHID WAFEFL LIVEGALTEM CEIPEMBOHL VERLIGGHULF WMDRIGHEHL
    CI MENTYYGURL SAIQAGTREE LYLHSLKLGY CONLIGRAFS EDDORGORF
   101 SWENGLALYLL ALRANCEFVR GHEGORLVSQ LEWFLEDERR AIDTAAMASL
   151 APT LERGNE MEGREOPITM AIRTVEREIL KAÇTPEGHEG NVYJTELALQ
   201 FLMTSFMEGA ELGTACLKAR VALLASLQDG AFQNALMISQ LLFVINHKTY
   251 ICHTEPOCLA PRVMLEPAAE TIPOTOEIIS VTIOVLSLLP PYROSISVIA
301 GOTVEDVLKE AHELGGETYE TOASLSGPYL TSVMGKAAGE REFWOLIPOP
   351 NTPLLQGIAD YERKDGETIE LELVSW
 (SEQ 10 NO:3)
 FEATURES:
 Functional domains and key regions:
 PDOCUODOS PSOODOS PKC_PHOSPH GRITE
 Protein kinase C phasphorylation site
Number of matches:
       1
               75-77
                             SLE
              174-176
                            IV:
PDOC00006 PS00006 CF2 PHOSPHO MITE
Casein kinase II phisphoryla in site
Number of matches: <
       1
               57-55
              90-93
                            SELD
             174-17
                            T7FE
             226-223
                            SLĮD
            249-911
                            T/10
             302-335
                            STVE
PDOC00008 PS00008 MUFISTYL
N-myristoylation site
Number of matches:
              1.2-1.1
                            GYLIGAL
               57-62
                            GLELSS
              € E-9:
                            BRAFSE
             149-154
                            GLAFTC
             190-19
                            G!IVYST
             209-214
                            GAELGT
             230-205
                            GAF INA
PDOC0009 PS00009 AMIDATION
Amidation site
             162-165
SignalP_results:
 Measure Position Value Cutoff Conclusion
 \text{max. }\mathbb{C}
          19 0.602 1.37
                                    YES
 max. Y
            19
                     0.702
                            1.34
                                    YES
 max. S
 max. S 5 ).974 ).88 mean S 1-18 ).949 \cdot ).48
                                    YES
                                    YES
Most likely cleavage site between pos. 18 and 19: ALT-EM
BLAST Alignment to Top Hit:
transpobalamin II, TC II [human, endothelial cells,
            Peptide, 427 aa] org=human /taxon=9606 /dataset=hraa
            /length=427
          Length = 427
Score = 732 \text{ pits } (1870), Expect = 0.0
Identities = 376/427 (88%), Positives = 376/427 (88%), Gaps = 51/427 (11%)
Frame = +1
```

Query:	.*	EBHLGAFUFLLGVLGALTEM JEIFERDCHLWEFLGGHLLFWMFFLJGEHINDGIYGGLFI	21.1
		MERINAPIPILIGVIGALTEMORIPEMOSHIVEKI.GQHILLPWMORLSIRHIMPOTYUGIRL	
Shir:	!	MERICAFLEGICALGALTEMOETPEMISHLVEEL QHULFWMERLSIERINESITY SLEL	$\mathcal{C}_{\mathcal{A},\mathcal{A},\mathcal{A}}$
Query:	2 1 1	GULÇA TEEDLYLESLELGYÇÇCLLGSAFSEDLGOGÇGEPƏMƏQLALYLLALRANCEFYR	15.
		SCHÖMCLREDTATHSTRICATÖÖCTTCRAVAREDDER ÖRLE WAR VARVATA FRYTRAMCHANK	्रञ्ज्
Sbjet:	£1.7	STORY JAKEDI ALI BELKIRANDOGI 1 OBE BARBBARAD SABBARA SI PERFRANCELAK	
orbjet.	17.2	GALQAGTKEDLYLHSLKEGYQQCLLGSAFSEDDGDCQGGGUNGQLALYLLALRANCEFVR.	120
Query:	3.41	GHEGÜRLVSQLKWFLEDEKRAI	100
		GHFGLRLVSQLKWFLEDEKRAI	4 .75
Sbjct:	121	CHFGDRLVSQLENFLEDEKRAIGHDHKCHPHTSYYQYGGILALCLHQKRVHCSVVDKLI,	100
		WE ASSERT THE PROPERTY CHEMICAL LIST OF THE PHONE OF THE SAADKE!	180
Query:	457	DTAAMAGLAFTCLKRSNFNPGRRQRITMAIHTVREEILKAQTPEGHF	597
		DTAAMAGLAFTCLKRSNFNPGRRQRITMAIETVREEILKAQTPEGHF	55.
Skjet:	181	YAVEPFHQGHHSVDTAAMAGLAFTOLKESNFNPGERQRITMAIETVEEEILKAQTPEGHF	240
		otal garages and the state of t	240
(wery:	598	GNYYSTPLALOFLMTSPMRGAELGTACLKAR VALLASLQDGAFQNALMISQLLPVLNHKT	277
		GNVYSTPLALOFLMTSPMRGAELG FACLKARVALLASLQDGAFQNALMISQLLPVLNHKT	7.7.1
ibjet:	241	GNYYSTPLALQFLMTSPMRGAELGTACLKARYALLASLQDGAFÇNALMISQLLPVLNHKT	200
		TUBERT A TRANSPORTER OF THE CONTRACT OF THE APPROXIMATION OF A PRINCIPLE A	200
[uery:	778	YIDLIFPDCLAPKYMLEPAAETIPQTQEIISYTLQVLSLLPPYFQSISVLAGSTVEDVLK	957
		YIOLIFPDCLAPEVILEPAAETIPOTQEIISVTLOVLSLLPPYFOSISVLAGSTVEDVLK	2.0
Sbjct:	301	YIDLIFPDCLAPEVMLEPAAETIPQTQEIISVTLQVLSLLPPYFQSISVLAGSTVEDVLK	360
		The state of the s	200
luery:	958	KAHELGGFTYETQASLSGPYLTSVMGKAAGEREFWQLLFDPNTFLLQGIADYRPKDGETI	1137
		KAHELGGFTYETQASLSGFYLTSVMGKAAGELEFW(LLEDPNTFLLQGIADYRPKDGETI	113/
Bbjat:	361	KAHELGGFTYETQASLSGPYLTSVMGKAAGELEFWQLLEDPNTFLLQGIADYRPKDGETI	420
		Z	420
luery:	1138	ELRLVSW 1158	
		ELRINSW	
3bjct:	421	ELRLVSW 42"	
(SEQ II	NO: 6	5)	
HMM res	ults		
Model		scription Score E-value	N
PF01122	. Euk	Caryptic cobalamin-binding protein 329.9 8.6e-246	_! <u>\</u> 2
CE00052		00052 lymphocyte_transmembrane protein KAP 3.2 2.9	1
			1

	Description	Score	E-value	N
PF01122	Eukaryotic cobalamin-binding protein	829.9	8.6e-246	2
CE00052	CE00052 lymphocyte_transmembrane_protein_KAP	3.2	2.9	1

# Parsed for domains:

Model	Domain	seq-f	seq-t		hmm-f	hmm-t			E-value
CE00052	1/1	1	11	[ .	1	11	[.	3.2	2.9
PF01122	1/2	1,	142	[ .	1	143	[ .	296.0	4.6e-85
PF01122	2/2	143	37.6	. 1	197	450	1	531 8	4 80-156

```
Isciorm a:
    ! MRHLGAFLEL LGVLGALTEM CEIFEMIGHL VEKLGQHLLE WMORLSLEHL
   51 NPGIYOGURE SSEQAOTEED EXERSIMEGY QQCELGSAFS REPORTQGEP
  101 SMGQLALYLL ALRANWHORK GHPHTSYYQY GLGTLALCLH QEPVHOSVVD
  15° KLLYAVEPEH ÇÖHHÜVETAA MAGLAFTÜLK RONENFORRÇ RITEAIRTUR
  201 BEILKAOTPE GREGNVYSTP LALGELMTSP MRGAELGTAG LKARVALLAS
  251 LQDGAFQNAL MISQLLEVLN HKTYIDLIFF DCLAPRVMLE PAAETIPQTQ
  201 ETTSVTDQVL SLIPPYRQGI SVLAGSTVED VLKKAHELGG FTYETQASLS
  351 GPMLTSYMOK AAGEREEWQL LEDPNTPLLQ GIADYRPKDG ETIELELVSW
(SEQ ID NO:4)
FEATURES:
```

## Functional domains and key regions:

PDDC00005 PS00005 PKC PHOSPHO SITE Protein kinase C phosphorylation site 198-200

PDDCD0006 PS00006 CK2 PHOSPHO SITE Casein kinase II phosphorylation site Number of matches: 7

1	67-70	THED
2.	90-93	SELD
-	147-150	SW D
4	198-201	TWF E
Ε,	250-253	SLÇĐ
6	273-276	TY1D
	326-329	STVE

PD1000008 PSCC008 MYRISTYL

N-myristoylation site

Number of matches: 7

12-17	GVLCAL
57-62	GLFLSS
85-91	GSAFSE
.73-178	GLAFTC
21.4-219	GMVYST
233-233	GAE LGT
254-259	GAFÇNA

PDCCCOORS PSCOCOS AMIDATION

Amidation site

186-189 PGFR

PDCCC0428 PSC0468 COBALAMIN BINDING Euka: yotic ccbalamin-binding proteins signature 165-178 SVI TAAMAGLAFTC

### SignalP results:

Measure	Position	Value	Cutoff	Concl	us:	ion		
max. C	19	0.602	0.37	YES				
пак. У	19	0.702	0.34	YES				
max. S	5	0.974	0.88	YES				
mean S	1-18	0.949	0.48	YE.3				
Modst lik	kely cleava	ge site	between	pos.	13	and	19:	ALT-EM

#### BLAST Alignment to Top Hit:

>CFA|108000024636236 /altid=qi|298316 /def=qb|AAB25526.1| transcobalamin II, TC II [human, endothelial cells, Peptide, 42/ aa] /org-human /taxon=9606 /dataset=nraa /length=427 Length - 427

FIGURE 2, page 3 of 4

Searce The Hits Coder, Expert - 0.5 Identities = 399/427 (33 ), Positives = 399/427 (934), Gaps = 27/427 (6): MPHLGAFLFELGVLGALTEMTEIPEMDSHLVERLGQHLLEWMDRLSLEHLNPSIYVGLRL 69 Query: 1 SERLICAFLELLGVLGALTER EIPEMDSHLVEKLGQHLLPWMDRL3LEHLNESIYVGLRL Bbjct: I MRHLGAFLFELGYLGALTEMCEIPEMDSHLVEKLGQHLLPWMDRLJLEHLNPSIYVGLRL 60 Query: 61 SSLQAGTKEDLYTHSLMDGYQQGLLGSAFSEDDGDGQGKPJMGQLALYLLALRAN---- 115 ISLQAGTHEDLYTHSL LUYÇQULLGSAFSEDDGDCQGKP3MGQLALYLLALRAN Sbjot: 61 SSLQAGTHEDLYLHSLKLGYQQCLLGSAFSEDDGDTQGKPJMSQLALYLLALRANCEFVR 120 Duery: 116 -----W-----W------HDHKGHPHTSYYOYGLG:LALCLHDKRVHDSVVDKLL 153 ₩. HDHKGHPHTSYYOYGLG:LALCLH)KEVHDSVVDKLL Sbjot: 121 GHKGDRLVSQLKWFLEDEKRAIGHDHKGHPHTSYYQYGLGILALCLHJKEVHDSWVDKLL 180 puery: 154 /AMERFHOGHHSMDTAAMAGLAFTCLKRSNENPGRHORITMAIRTMEHCILKAOTPEGHE 213 ZAMEPFHÇGHHSMDTAAMAGLAFTOLKESNENPGEKQRITMAIRTMEEILKAQOPEGHF . bjct: 181 (Avepfh@Ghhsvdtaamaglaftclkesnfnpgrk@rithairtvfeeilka@mpeghf 240 .uery: 214 GNYYSTPLALQFIMTSPMRGAELGTACLKARVALLASIQDGAFQNALUISQLLEYLNHKT 273 GNVYSTPLALQFLMTSPMRGARLGTACLKARVALLASLQDGAFQNALHTSQLLFVLNHKT Dbjot: 241 GNVYSTPLALQFIMTSPMRGAELGFACLKARVALLASLQDGAFQNALMISQLLPVLNHKT 300 query: 274 MIDLIFFICLAFF, MLEPAAETIP, TOELIS VTLOVLS LLEFYFOSIS MLAGSTVEDVLK 333 YIDLIFPECLAFEYMLEPAÆTIPOTOEIISVTLOGLSLLFFYFOSIJYLAGSTVEDVLK Cbjet: 301 YIDLIFPECLAFFYMLEPAAETIPQTQEIISVTLQVLSLLFFYFQSI3VLAGSTVEDVLK 360 .uery: 334 KAHELGGFTYETÇASLSGPYLTSVHGKAAGEREFWQLLRDPHTFLLCGJADYRPKDGET1 393  $KAHELGGFTYET \\ (ASLSGPYLTSVMGKAAGEREFWOLLFDPNTELLOGIADYRPKDGETI$ . bjot: 361 KAHELGGFTYETQASLSGPYLTSVNGKAAGEREFWQLLRDPNTFLLQGJADYRPKDGETI 420 .uery: 394 ELFLVSW 400 Sbjct: 421 HLRLVSW 427 SEQ ID NO: ")

#### HMM results:

	Description	Score	E-value	N
	Eukaryotic cobalamin-binding protein		8.6e-269	
CE00052	CE00052 lymphocyte_transmembrane_protein KAP	1.2	2.9	1

#### larsed for domains:

liode:l	Domain	seq-f	seg-t		hmm-f	hmm-t		score	E-wallue
(E)0052	1/1	1	11	{ .	1	11	[ .	3.2	2.9
FF01122									
PF01122	2/2	117	400	. ]	145	450	. }	660.5	8.76-195

```
1 ATATGTATOG GAAATATGUT GTOTTESTAT TEOTAGOGO O GGASSITOTA
                        51 G RITGAGT CASSTAGGTA GGCAGGGGG TUTTING TO GTTACTTOG
                  101 A COCCAAC TE CTCCCGG ATCAGAAGIG ACTCCCCGG AGGATGCTGC
                                                 DE TI TANCO CARAGOCTGA CGATAACGAA ACCTATUDEN LAT GODA C
                 201 10 5
                                                                                    DG TO TO TOOTIG GARATAGGRA TOATAATA TO TOACTGOA
                  251 IV A RA A GC ITOGGGG AG AN RIA PROCEAUDIA GCA AAGET
                                                 TO THE ATTIC OF ACTOTTO ADDITIONAL ACCURAGED COMPARISON OF
                                        OTT TOO G AF STEGGET CO AC TO STEETS STATE OF A SAACC LOCAL CONTROL CON SAACC LOCAL GOOD TO THE SACE ACT OF A SACE
               461 TOTAL ARTIT CARRETTED A FILET ES LABADAGARA CEUNTERSTS
               EDI CATTI STITA TOE AAGGGO TIG TILLIS ATAAGTSANG CIGALANAGA
EDI STOT STAALA SCA IGAAGO TIG TAALIF ASJATAANAT AATIGDNATG
               601 ROATIOTOC DE ARATOA TEGRADATE TITAAGGIVA TEGTOT TEG
               COL ADMANDERS OF MANAGERA ACTIVITIA NA FRATOTTICO TRACCETORO
              701 ADOLMACA CAAMAADA TULAAA ID AGAGSTIAA GOGACDTOGO
701 MAANGUACA A MAGADA TAGITAA ID GTATACAING ATTOTOGOT
               9 H GO-9010 HOU ACATHADGAA BUDDINGTID OUTTOOCIGT TIGGRAMANT
               BEL TITITITEDAS GIORMITOS GARTIONOGO GASTAGOROT GETTOTOSIA
               A 01 PACTURED DE CONTRACTORAT CHUNTTOTOR MURATTETATT MIATTETERA
F-1 PACAMPUNCO MACCITTORA DU BASOLIAS ANTIGOASTOS CUTAMPOLIS
      19 1 STIATICA SCIPCART TERRORT A ALEGATORIC CISCITCARD
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 $14.2^{\circ 4}$  homeodico incidentados (algoridade designamento esta estado 142% Испольной принименний плинименний и имплиний минелимени 14331 исилияния исиминики исиминики иченикий иченикий виминиями виминий принципри видиний ви 144)1 киниципин пирикинки киниципин каниципин 144%1 киненияни инклинения иниванияния мананияния иманамания 14501 МИНИВИМИ ВИБИНИВИИ ПИВИЛИВИЯ ИЗВИВИВИМИ В ВИВИМИМИ 14551 МИМИМИНИ ПИПИМИНИ ВЕПИМИНИИ ИЗИМИМИНИ ИМПИМИНИ 14001 ининимици кикинимин: икинимини изинимини имкинимин 14651 иминикини кисиминин смининими имининим иминими ницииниции импиниции иминандиим пенцииниции пенцииниции 16751 14801 импиними иниминими иниминими изиминими изиминими  $14 \odot 1$  инивинини инивининин инивинини иливинини иливинини 14%51 иниминини иниминини иниминини изимининин изимининин 15(-)1 ИНИМИНИНИ ИНИМИНИНИ ИНИМИНИНИ ИЗИВИНИНИИ ИПИНИМИНИ 15001 иниципин иниципин иниципини иниципини западанини 15. 1 импиними миминими мимимими миминими инминимими 15: 1 инпиними иниминими иниминими иниминими эниминими 152-1 иниципини иниципини иниципини иниципини иниципинини 15/01 иниципини иниципини иниципини ппиниципи 1947 Г. ИМИНИМИН ИМИНИМИНИ ИМИНИМИНИ ПИПИНИМИНИ ПОВИТИТЕЛЬНИ 16401 инининин инининини инининин инининини инининини 10001 иминимин киминими иминимини иниминими иниминимин 150-51 иминимин имимимини имимимини пинининин пинининин 15%/1 иминимин имимимим имимимими иниципими иминиципими 158: 1 иниципина иниципини иниципини принципини иниципини  $1^{\mathrm{opt}}$  1 имининин имининин имининин ишишинин ишишинин 160 (1 импиними инминими минимини принципини иниминимин 160% 1 иниципин иниципин иниципинин иниципинин иниципинини 163/4 иниципини ишининини имининин ишининини ишининини 1611 гипинийний иминийний киминийнийн инийнийн инийнийн 16211 инининин инининини инининин инининин инининини 16701 иниципини иниципини иниципини иниципинини 162/1 иниципини ириниципин иниципин иниципин иниципини 16401 иминимин инминимин миниминин шишишиши шишишиши 16451 иниципини ишининини приниципин приниципин приниципини 163 (1 импимими имимимими имимимими имимимими имимимими 1666 1 инипинини инининини инининини шининини шининини 16301 иниминии иниминиии иниминии плинии плини плинии плинии плинии плинии плинии плинии плинии плинии плинии п 168! 1 импиними импиними кимимими иниминими иниминими 11001 иминимин иминимими миминими иминимими иминимими 17101 КИМИМИНИИ ПИМИМИНИИ ИМИМИНИИ ПИМИМИНИИ ПИМИМИНИИ 17201 ИНИМИНИМИ ПИМИНИМИНИ ИНИМИНИМИ ИНИМИНИМИ ИНИМИНИМИ 17451 ИНИМИНИНИ ПИМИНИНИИ ИНИМИНИНИ ПИМИНИНИ ПИМИНИНИ 17551 инипинини инипининин инипининин инипининин инипининин 17601 ИМИНИМИН ПИМИНИМИН ИМИНИМИНИ ИМИНИМИНИ ПИМИНИМИНИ 17651 ИНИИМИНИИ ИМИМИНИНИ ИМИМИНИНИ ИМИМИНИМИ ПИМИМИНИМИ имининии инмининии пинининини пинининини пинининини 17771

17751 иштанату анаташын татыштын иштышты иштышты иштышты 17801 иниминикан ишканикано иминимина палиминано иминикания 17851 илиполици видининим взапенемым чининения вивопинии 17901 инпиниямие инивидиями винексмены эксплинисти пиниминици 17951 инпиниции испиниции испиниции принципини пиниции 18671 пиминия иниципации применения применения применения применения 10001 1 051 иншининин иминиминин шиниминин эмилимини индининини тамийний индивиний принцинципринципринципринципринципринципринципринципринципринципринципр .51 ининенный импинийный панинийный импинийный импинийный 1- 01 миниминий иниминими иниминия эниниминий инэминий 51 кимилинин билининин какининин лимининин имлининин  $1\cdot\cdot 01$  ининсимини имилимини имиминини лимининини инлиминини и -51 минисини иничинини инипинини инининини инининини 1-401 миникинии инпининии инпининии пинининии пинининии 1- 151 иниверини иниверини иниверини иниверини иниверини иминиции иминици иминиции имин 1-351 иминамими минициими минимимим иминимими и иминимим 1-- ) 1 пинициины биндининин энстичинин зипининин педагличин  $1 \cdot 1 \cdot 1$  принципина системника инципинина принципинина принципинина инципинина принципинина принципина принцина принципина принципина принципина принципина принципина принцина принципина принципина принципина принципина принципина принцин  $1 \times 7.51$  пенениення явинимими инбививимим инпививими пененимимими 1 - год парынышим мининаным мининымим иншининым иншинини 1: (51 шишиния пинишини иниминины инишинини инишинин 1 < > 1 инпиними импеними импеними импенимими инпенимимими  $1^{-3/2}$ 1 ининимини имисивини имиминини импенинини исплинини 1.2.201 инепринции импининим импиними империтими изининини  $1 \cdot \cdot \cdot 51$  кимпениции пененения инпивимыми импениции киппениции 124/4 ининеризии принцинини намининини электичении минининини 19191 пимениции импенения импиниции пимениции верешении 19. О БИБИБИВИН ИБИВИБИБИ ИМБИМИМИМ ВИБЬИМИМИ БЕБИБИВИКИ 19251 изминации иницивимым имимимыми имимимимим киниципимим 19301 причения приспечения преминени инференции веренции 19751 Ирминиции инминиции импиниции пиниции инминиции 134-1 применения инприника вкраинкам пиривидими вестыпным  $1^{5}4!1$  мибементин имперации имперации имперации еценициим т.е.т инпримени пиримении пиримении пиримении пиримении учетельный 1 - c ) 1 Ruburheum underenden underenden underenden einemenn  $1 \oplus 61$  Kunenheuen demeneren unmneneren enrneren kemereren 13 01 KUNERKKUND UKNMENENIN UNUNNINGEN UNKKENDEN KUMENMENEN  $1^{\pm}$  .1 инменители инвигивний инвигивний инминивний виминивний  $1 \cdots 1$  remembered envendement envendement hundenvend kreekenen 1 + 51 unnunulun unnununun unnununun unnununun unnunununun  $1 \pm 0.01$  испинийни сикимимими имимимими бинимимими имимимими 13051 CHEERUREEN HEKKENNANN ENANNANN ENKNENGERN ERKEKKINEN 2.001 пенепинени империнини пинининин пининини империнини  $2^{\frac{1}{4}-3}(1)$  империинен инферитурания инпервый инпервый инпервый инферитура 2:1 (1 пристипни рипкличий приминий приниминий принимин 23.51 DENEMBRAN CHMANNANA MANANANAN MANANANAN ARECEARTO 2 1 +1 AACCABITSC ATAAATCAST COLSTATOTT COTTEGGGTG GAAAGIGGAT 2: 51 GOBAGTTAIA ATTIBABTIC TOTTTTGTOT TAGTOCAITG AABCIBCTAT  $2 \sim (1)$  TA CAAAATAC ÜATAAACTIGS GESGOTTATA AAQAGCAGAA AIGAGGOOG 20 M.1 GEBORGTORO ICAIRCOTAT RAFFOCARDA GITTERRARG CORAGROARS 20 40 1 TEGATUATOT DAGATCAGIA GITDAAGADT AGCOTGADIA ACAIGGTGAA 201/1 ACCOPSTOIC FACIAAAAAT ACAAAAAAIT AGCIGGGGT GGIGGCGGGC 201 (1 ACOMBRANC COASCINACIO ABBAGGOTBA GBCABBABAA MOSCITTGAA) 20041 COASSAGEOG CAGETTECOS TEASCTGADA TOADEDCATT ECATTFOAED 206-01 OTEGGCACAA AGAERGAAAS TOCATOTOAA AATGAAARAA AATAACAGAA 20041 ATGRATTICT TAACAGETOT GGAGGTTGGG TGGGCAGETOC GAGATCAGGA 20101 CADITSACABA TIPCAGISTOT GATGGGGGCC CACINITORSG TETPACOISC COMPLETES CONTROL OF CARACTES OF GRANGEACOM FREGUNDA OF THE SERVICE OF THE SERVIC 20-01 GITTIITAAT ITAAAAAAAA AAAATATTII COTGIOCOTT 20:51 GBAACCIOTI TIATAARBET ACTRAAAAAF TITTERTTTT GAGATBBBB; 20 ml topca of the modeledge transposet afcadament carettach; 20 ml caacotoffe erdochfesch transposation becauche georgefear 21 01 TACGESTRAD CATAGGECCA TGG DACARAG COCAGUTAAT TTOTTREAT 21: 1 TTTAGTAGAA AIGTGGTITC ACCATGTTGC ATAGGUTGGT CTUGAACTIU 21: 1 TGAACTCAAG TGATCTGCCT GCCTTGGCCT CCCAAAGTGC TGGACTCTA 21131 GGTATGABOC ACCORGATOG GCCTATAATG GUACTTTOCT AT BUCATTBA 21 1 TGAGGUTOTA CTOTCATGAG CTARTCATCT COCAAAGGCC CTAAGGCCTO 21211 CTGATACCAT CACCTTTGGG GTTAGGTTTT AACATATACA TTTT3GGGGG

FIGURE 3, page 7 of 22

1-1 Tiraterra Garagaaret Tabelature Goldari 14 98914 WAIS GTA: WIST ARITS TOT AART TRACK IN SERIE AAR FROM 4951 COTOSCITA E COTOCOCAGT ACCTGOSATT A MOCCATGA ACCASSACA TORINATE TERRETTE ANTAMATA SCHEET TE ATTEMEN asal gostostal gametasam tememberga tetasatal tesas etti. - I AAANTA TURI HATTAHA 1000 PEHABAHAHT SILPIUTHUSI JA PUOHA IS PIFI GNOTTITAAG AGGETTÖCTG TGG ÄGTUGU ATHEAGAGUG ACTHEAGAAA TI MAN TITE AND CLASAN OF TAR SAN GOVERNING. ON SILVAGA PS251 GTPTCTTGG: TGQCAGGGCC AGAAACGAA GT HAAROCT FT HACAAGA 1991 GUDHARATAN AN ATOTAGA ATMAGAGAGG AGASTRAGO NETHAGASIS UN351 GAGAAGASUG GAATGOMACT BAG GAMAGA GAMMDA MTGA MAMTGOMAGG 5411 Participal inceptions Arganologic biginititist at Calibbit 25451 CACCCTUTCT CGTTGTACAT TGTACACATT CTAGGTGACA CCACCAGGTT .5501 UTGATTITCA TOPOCCATAA DATDAGOCOO OCAGAGAGGG GAMAACTGOT 75551 GAG TGATAA CATAATAGAT BOODCTTTOO TGGAGG CAT GGTCATGGTC 29601 AS NOTOGAÇA GGATGANGCO FGASCAGGSA GGATCGGGGG FOTAGAGGGG 25651 AAGGAGGTGG AAGTTGAGAT CACAGACCTG TGGTCAGGTG GCCTGGGAAG NOGI GGTITGAUGA GTGTOGGUOC AAAGAGATTG GAAGGGATTT TGCTGCTGTS 25751 GGTCAGCACT GCCTCTCCCC TTAGGGACAA CAGCCACCTC TTCTCT 0000 28301 ATTIGOUTIT COUTTOTGTA GATATGAAAC ACAGGOSTOG TIGUCAGGOS 25851 CCTACTTAAU CTCCGTGATG GGGAAAGCGG CCGGAGAAAG GGAGTTCTGG 20401 CAGGITOTOL GAGACCOCAA CACCOCACIG TIGGAAKKIB AGIKATGGCC 25951 TGA ACTOTO GATOTGTOCC CTACCOCAAG CTTACTCAGO CAAGAGGCTT 25001 CATCAACTCA COCCAGOTTT COCTAGCACC CTOUTGEGEC ACA ETTCAC 28051 AAAATCACTO ATGOTCAAAG TIGGATATAA TATATIGAAC TGAAGCOTTA 20101 GCATTTTAT GCAAGTTACT GTGGAAATTC TAGGAAAGCA GAGAGATTAG 20151 AAAAAAAAA AAAAACTAGA AGAAAATTAA CATCACCTAG GATATACTAC 16201 CTAGGAATAA CGTCTTTTAT TTTGAGATGG AGTTTCGCTC TTGTTGCCCA 26251 GGCTGGAGTG CAGCGGTATG ATCTCGGCTC GCTGCAACCT CCGCCTCCTG 2e301 GGTTCATGTS ATTCTTCCAC CTCGGCCTTC CTAGAGCCCA AGTGGTCTGC 2c401 CAGCCAAAAT TACTTAACTT TTCTTCTAGA TACTTTTTAA AAATATGGCA 26451 GTAAGTTTTT CATAAAAAAT GGAGCCATGC TATCCACTGG AAATTTAATG D6501 TTGCCCACAT GTATAACTTA AAAATTTCAT ATATGTGTAT ACATATATAT 28551 GAAMTATATA TATACAGACA CACATATATA TGTATACATA TATATACACA 28601 TATATATGTA TACATATATA CACACATATA TGTATACATA TATATACACA 20651 CATATAGACA TATATAGACA GAGATAGATA TATAGAGAGA CATATATAGA 20001 CACATATATA CACACATGCA CACATATATA TGTATACATA TATACACACA DE 151 TGTATACGTA TATATACACA CATATATACA CACATATATA TACACACATA 2x591 TACHCACATA CACACACATA TATACACACA TATATACACA CATATATACA 18-51 CACATATATA TGTATACATA TATATACACA CATATATACA WATA MACACA 2000 TACATATA CACATATACA CATATACACA CACATATACA CACATGTATA 28951 CATATATATA BACACATGTA TACATATGTA TACACACABA BATATGTATA 27001 CATATACA CACATACATA TGTGTACATA TATACACACA TACATATGTA 17031 TACATATATA CACACAT ISEQ ID NO:5/

#### FEATURES:

Emon: 0031-0034 Intren: 004-5664 Emon: 5570-5760 Intrên: 62-3-3671 75100-7741 Enon: Intron: 7742-10000 Emon: 10041-10173 Intron: 10174-10298 16099-10485 Enon: Intron: 1048e-12027 10008-10193 Enon: Intron: 12194-25821 25822-25939 Emon:

#### Allelic Variants (SNPs):

AHO				Protein		
Position	Major	Minor	Domain	Position	Major	Minor
951	C	T	Beyond ORF(5')			
137.1	C	T	Eeyond ORF(5')			
1.85.0	G	À	Ee ond ORF(5')			
2859	A	+;	Intron			
31.30	G	Ž.	Intron			
6621	G	Ä	Intron			
4) (+2) E	-	A	Intron			
HIT 2	$\mathcal{F}_{i}$	T	Intron			
4 = -	G	is	Intron			
	Τ.	Żs	Intron			
80.65	T	C.	Intron			
81 L.1	O.	Ţ	Intron			
01 f è	G	C1	Intron			
915 C 2	C	1	Intron			
4. 85	G	20	Intron			
	Ğ	A T	Intron			
.116(	$\mathcal{A}_{i}$	13	Intron			
13086	'Γ	+1	Intron			
1.31.83	T	4.1	Intron			
111140	C	+;	Intron			
1.14 0.6	A	(**)	Intron			
212 C5 E	C.	Ä	Intron			
22.233	C	Ä	Intron			
21245	C	-	Intron			
7.7 : T.	C	7	Intron			
112 (42	A	· T	Intron			
21: 3:44	Τ	<b>C</b> 1	Intron			
213 8 7 3	A		Intron			
24764	G	T	Intron			
114419	T	10	Intron			
7464	G	ž <sub>A</sub>	Intron			
345 C 942	C	q.	Intron			
215 42 8	Τ	1 3	Intron			
11.011	C.	T.	Intron			
25484	Ç	J.	Intron			
1161.65	A	-	Beyond ORF(3')			

Context:

Position

921

'TTGGAGATAT'I'TTAAGGTCATAGTGTCTTCACAAATTGAGCTGAAAGGGAACTGTTAGGA TGATCTTGCCTAACCCTCTCATCTCACACAGGAAGAACTATTTTAAACTCGAGAGGTTAA GTGACCTGGC::AAAGTCACACAGCCACCACTAGTTAACTCGTATACATTGATTCTCCTGT GTTACTTTCCGAGTTCTGGCAAGTACCCCTGCTTCTGGTAGCTTTGTGTCTCGATTCAAT [C,T]

TCATTCTTTTTATTTTATTTTTTTTGAGACAGGGTCTCACTTTGTCACCCAAGCTGGA  $\tt GTGCAGTGGTGTAATCTTGGCTCACTGTAGCCTCCACCTCTTGGGTTCAAGCGATCCTCC$ 

FIGURE 3, page 9 of 22

TERREPARCICIONA AGTAGOTOGGATTA CAGACOTOTOGUNACIANOS AGUSTAATTTA TUUTTETETTOTATO OUTTITTETGTTTE: "TAGACACACAGTGTTTO OU ATGITGOCOAG GEPROTOTOGAANT OUTGAGOTOAAGTGAUNTENCOON OUTGAGOTTITE AGAGTGOTAUG

30 OFAGGIGO \$1A TARRAS PAGRETO TO EROTAMBA ATARRAS \$TAGRAMAN ANTO COCCAA FROM SOME TERRAS AND ARRAS AND ARRAS AND ARRAS AND ARRAS AND ARRAS AND ARRAS ARRAS

CONTROLOGICA DE PARA CONTRE ENA VALERA SIN STRVATT DELA SIGATIVA A HACITA AT CA DE SA DA GUARDA DE PARA EN ENCENTRA AL COUTRA ROMA DE PARA DA REGIONA EN ERCA SO A DESCRIBADO DE PARA MENTE EN EL CONTROLOGICA DE ROMA DE CALONDA DE PROPERTA DE SA A DESA DE DA DO DE PARA CONTROLOGICA DE PONTROLOGICA DE RESPONDE DE LA CONTROLOGICA DE PARA CONTROLOG

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FIGURE 3, page 10 of 22

DARATA ARAA LA PEGOTO GETGO GETCO COLO ACEGO O CARACO CAGO ACTETE EGO A ÉGO DAL GETACO LA GALCACI TERRO, EL LA COLO ACARA COLO SECO DA CATACO DARA COCTETE DIA DIGARRA TACARRARA PURCECARRO DE EL COLO DE POGO ARA ESTRA TOC DAGOTA DI POSO SAUGCO CAGGO AGRAGA CARO COLO PORA ROCO DE LA COLO DE LO COLO DE LA COLO DE LA COLO DE LA COLO DE LA CALO DEL CALO DE LA CALO D

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FIGURE 3, page 11 of 22

SHADWAATI GUNAGUGUT AT HACT WITCH DAGUTGT VAGUTGT VAGUTTIIGGA KUTHGT A HILL AT TOTAL TO A HAR IT WAS WORK STOPEN SO AT TOTAL TAKE AATAAJAAAGTTAGOOGGGOATGGTGG TACAT BOOTGTAGTTQCAGGTACTQCGGAGGOT ga 14 15. ga gaat la titurado 193 gabeno algo 193ag daginastiga katologa lia 3.3.40 GRADUR TO CORDECTE TRACTA PER ATATOM OF GRANTS TO ADMICTOR A CHAGAAGG BOSTOCAT IA HAGGUENHUTGDAHAAGTE OTGEATGOTHTGGAADUTTT I DA TAGGE CAPCATTOT TERRIT METAGETTA DE RITOR DARROLLOGITS PARTICO CTM AG POO MAGGTOTO DAMTGATGA HOTOMATANDE EGO DOO MA LACTIONO METER EN TOUGG TOOT COGAAT GAAGTO HIT PARGGAD GAATTIGGOORGOOT CAT COGTOAT GOT 3.1 CAGCTOT GÁĞCONGOTTT EGAC DIYOĞ HAĞQIYĞ DATOTOTT BADĞCONG BADETOAA BAÇA ACMIGNIBAACONCATSI NIA NIAAAAATAAAAACITABI DEBENINGI EGILADATE CUTOTAUT JOCA JOTACT EGGGAGG ET BAG MEAGGAGAAT JA ET FGAA DE PRIGGAGG IGG DAGITERATIK ADAGAAN DEGINOOPAGOTI OO DISTAA DAGAA FAAA FAAGITAA G ACT TTGTCTCAAAAAATAAAAATAAAATAAAATCCCCCTAGTGATTCCAATGT /CAGCT 9782 CONTENTAGEO COAGCEACE DO GAGA SO FASCAGA EN ACETICA A DE GAGA SO A SEC GAGG DI OCAGIGAGIGGA BAIFC BUA DUNCI SICIDITO A BOST BOBCAADA BAGI DA BIFGA GAG FOTOT DTCA AAAAATAAAAATAA AATAA RACTOODO TA GT GATT DI AA TGT GDAGC TAA PITTI GOAAA PAGGI GUTA EGGGOT DAAUT DUTCH EGGOODT DOOT DUTD DAA EDDTT CTCCCTAACCTCTAGCCCTCAAGTIGCAGAGTGATCAGCCAAACGAGTTTGCCCAGAAAT [G, T]ago abiti toctobgacacacatti po ngaciti dagacaa boaaagitoti begcaba nca GGT1 3AGTTGGTGCCC (TAGCTGAI CT 3ACCAT GTTGC DC F1 CTTCTCCAAGCCC TC CTG TEGITGTCCATA SUTA "ANGGCCCTGA DOUTCAAGCCCCTGCCTGTCCT (G1000 F17GG CTCTOCAGOTCA PTGCATGTTCTGTCCCCCCCACTTCAAGACACAGCAGCCATUGCAGGTTT GGC A TTC ACCITG FOT GAAGCOCT CAAA UTTC AA DUCTG ST GGGA GACAA HIS SATUAD CAT 11493 RAARAAAAAAT GGAGAAGAAGGAAGC EGGACA EGGEGGCCCG EGCTTATAATOC EA GCA CTCT GGGAAGCT GAGG, AGAT GGAT TG CCTGA GCCCAG GAGT TTGAGA CLAGCCT GGCCA ACAI 361 GAAAC CCTGI CTTI ACTAAAATACGAAAGATTA 36 CAGGCAI +31 GGI AGACA COTA FANTOCCA SOTA/ TAGOGAGGOT BAGOCA DAACAAT DAGTIGAN DI FIGGA SA DAG AGGI PUCAGTGA SOCGAGATO GOGGICA PTGUAU POCAG DOTOG SOGAČA PROTIGA SA UTO ICTC I DUAGAAAAAAAAAAAGAAT GGAT AGAGTUGAGCCAA BAAGA BGCAGCAA AAACAAAGA CACA SAUSTRICA (ASA) TTTOGGGGGA TTTT GAGGAPT PSTOT PSCAAAA SAGTOGGATO TIGGGAGAATGAG TGGGAGTUGAAACCA BATGAATGAAGAGAAAGGTSAGG FBATCABGBTA ACADADAT SOSTTOTORACAATODAT BITOTA SOAR GAGOOO TOTGGA BI POID GGIGO CACAGAGAGGTGGGAGGAAGGATACTGGAAGCAGAGAAAACCAGTGAGGGGC (FGATCTTGGG ACAAGAAGAGAAATAAT COACGOTÜTÜTGTOO POACAOCAGOT PÖÖCGGOTÜ TTI OT POC 12260 TGG CACAGTCAT STTGGAACCAGCTGC FGAGACCATT CCT CAGACCCAA CACATCAT DAG TIGT CACCOTIGGA SCTOCTTACTOTOTOTT BOOGC DIGTACAGA DA STOCATOTOTICTT DIGGS CGGG FOLACOST SGAACATGT COTGAAGAAGG FOCATGAG FLAGGAGGAT FLACG FGAGA CTCCCACCTCCCAGTCCTCACCCCACCCCAACCTCACATECTCATAACAAGETCACAEAAA 2. [] AGAC BOUGANCA GAGGRIGACOGITICOS IL DESGRIGAGADA DAO LO EDDITE DI LITOTA COME OT CAGOTO OTTO TOTOCOCACEGITETT AT GGAA ACAEG GAGOCA DA GEOCAECATT GTCADIGAGABA PDAGGOTTI GGAGGOAGACO COCA, A GILIC GAA POODAA CITCI AA DDA GOTA SET TOCAS STAGOCACCACAATTCAL CHAGGAGAA (A STTISTIGO COL TTO DO DGO AGO: DEAGTGTGAAGN: TOCAGGACTTAGTAGACATAGAGATATAGTGGCATGTGCTTTTA GGCACITGOCACACAAA COTOGGTAATFTTTTTTTTTTTTTTTTTTTTTGAGATALGGTUTCTG 1308€ TOT PILOCOCAG SOTS STOTA AAATTOTTG POLITOAAA CONLOCT CACA LOLGAO SOCUT CAAAATATTGGGATTATAGGTGCGAGCCATCATGCTCAGCTAGAATAATAATTGCTTTTT TITI SINI TITI NI NIGAGACAGAGI CITCACIN, NATITACOCA SOCIOTIGGA EST CCAACING TGT I TSTGTATT PGTTI ATTTTTATTTATTTA FTTATTTO SAGACAGAS CUICTC PCTTT T. 11 ACCIAGGOTGGAGTGCAGTGCGCCAATCTCCGTTCACTGCAACCTCCGTTCCGTTTC AAST GATTETOORGOOT CAGCOTTOATGATTAGTOGTGCTACAGGOGGTTSCCAC CATGO  $\texttt{CCA} \\ \texttt{CTA} \\ \texttt{ATTTTTGTATTTTAGTAGA} \\ \texttt{GACAGGGTTTTACTATGTTGGGC} \\ \texttt{CA} \\ \texttt{CTGTTTTC} \\ \texttt{CCA} \\ \texttt{CTATGTTTTGGGC} \\ \texttt{CA} \\ \texttt{CCA} \\ \texttt{CTATGTTTTGGGC} \\ \texttt{CCA} \\ \texttt{CCC$ TAA! TOOTGAAC FOGGUTGATOPQUOTUGGTO EGUOTOCCAAAGTGGTGGGATTA DAGGO 13183 ACCATOCTCACACOTGAGGGGGCTCAAAATATTGGGATTATAGGTGCGAGCCATCALGCTC AGCCAGAATAATAACTGCTTTTTTTTGTTTTTTTTGAGACAGAGTCTCACTCTATTAC

FIGURE 3, page 12 of 22

FIGURE 3, page 13 of 22

THAS SOCKEDS TATES OF STRACT CARBOTON PROTOTS FROTTA SACTOR AS THE

CAGITTOTTGGC/CAGTAJO PUCCOGAGACITTAG JAGGGITGCT JAGIGCCTS ICTOT GA JAAAATTAAAG JAGI GALGGCITGTGGACCTJ ITA AGTGGCITGCTJATACTJ CTIJAGCTGCAGGGG/AGGG/CAAJAGAAGGGGGAAGTAACCCTAT JAGGGAGGAGTGGAG GGTGCTTGAGCCGC/AIGT/GGCACT JGGGGAGTJATGAGGT TGACTACTGACTGA/JA/O/ACTA/TATGACTGAJCACT/GJJAGATACTATCTTG

> CAGGARACTGGT SCT SAMMAGGMAANT SACTOAC (AAG 3 FCA SAGACTAGGCAGTGA F GCTGGGGGAACCTGHCTCAHAGGMHACAGACCTG SCCT SGGSCA SCCTTGCAGCTCCCC ACTAAAATACTGAAMATHAHAGGCTTGGATGATGAT TATAATCGTATCGCAGAGCCCCAA CTCAACTGGAGCCCTSCHAHSCANAGCCTAGGGT ST SACTCCCT SCTTTTCCACAAGGCA CCATTAGGGCATCACCCCAHAGCCTGGMAGCCASACGASAGATCCTGCCTCTCATPGG

23344 AGGAAACT GTGCT GAAAAA GGAAAAGTGACT A DCAA GGTCA GAGACTAGGCAGTGAT G CTGGGGGGAACCTGC CTCAG - SGA GACAGA TCTGG TCTGGGCAGCCTT GCAGCCTCCTCA CTAAAATA TGAAAATGGGG GGCCTCGATGAT GTTATAAT DGTATGGCAGAGCCCAA D TGAACTGGAGACCT GGGAGCTAGGCTAGGCTC TCAC TCCTT GTTT TCCAAAAGGCA D CATTAGGGCATCACCCCAGGCTGGCAGCCACGACGAGGGAT CCTGCCTCTCATTGG T

SUFFICIAGAGAGATA (FIRMA OTAA) CAACTITALAACATTECET TATATITUGG CCAGGT FC AATGGCTCACGT ITUTAATI DOA (FIGOTTIGG) A BCA DIA BA BA IDACTIGAG BTOAGA B TITOAAGA DIAG IDTIG FOLAACATATIG IAGAAACO CATIET ITA DTAAALATACAAAAATTA B CITOAGGC BTGGTGAT STIROACCT ITAATICITAGO TADIETA BA BACTIAAGGCACAAGAD T TIGCTTGA BTOAATATTIGIA (CACTIGOACCCT BIB GCAACAGGGAGACTITTGT DID TALIET

A TAGOT GENATINADA ESTADORA MAGNAT ECCAGO DITAR TELETÉS PATRATA ETA ETA ETA GATO E BORT TRADORA DES TRADORAS DE CONTRA DE CONTRA DE CAGO DE TORA ANTO DE CONTRATORA CATIGA SOCIACA DES TORTES DE PODE DE CONTRA DE CAGO DE TRADORA DE CONTRA DE CAGO DE TRADORA DE CONTRA DE CAGO DE CONTRA DE CAGO DE CONTRA DE CAGO DE CONTRA DE CAGO DE CAG

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FIGURE 3, page 14 of 22

TWO UT BE DUACOGASTITS ITTOTAL TOTTTTGAGATGGASTITTGGT LATGITGG IN AGGSTSUBGTAGATTGGTAGGATGTOL BUTGAGTGGL NIL TOTALOTGGGGST LAART

# FIGURE 3, page 15 of 22

GATGGA PETRO - DE EFETANO A DE GASTOS AS ESTADOS ATA ESARE DE CENTRA CARAGA SA ESTADOS AAGUSTOS AAGUST

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# Allelic Variants (SNPs):

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$\frac{1}{1}$ $\frac{1}{2}$	C	TITHOL	Domain	Position	Major	Minor
1: 2	C	ů,	Beyond ORF(5') Beyond ORF(5')			
1 - 1	G	À	Beyond ORF(5')			
2:10	4	G	Intron			
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5732	3	Is	Intran			
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173-61	A	G	Intron			
11167	7	C	Intr n			
1.1 4	-	C	Intr n			
2.5.1	Ĉ	G	Intr n			
231.96	ה	G	Intr n			
22.159	Ċ	T	Intr n			
21114	Ċ	A	Intr.n			
11346	Ċ	-	Intr n			
114"6	C	Т	Intr n			
2.7193	A	- T	Intr n			
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26140	(*) 	С	Intr n			
25046	G	A	Intr a			
25193	C	Ţ	Intron			
25 519	Т	G	Intron			
25614	C	T	Intron			
25735	C	T	Intron			
2€156	A	_	Beyond CRF(3')			
			4			

Context: DNA Position

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FIGURE 3, page 16 of 22

GTG AUTG TESTAAT TEGESTUA STOTAGEST SCARST STESTENGGET SAAG SGATSSTES

FIGURE 3, page 17 of 22

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[G,A]

FIGURE 3, page 18 of 22

GACTCTGTCTCAAAAAATAAAAATAAAAAAAACCCCCCTACTGATTCAATGT WAGC TAAGTTTGCAAAATAGGTGGTLTGGGGTCLLCCTCCTCCTGGGCCTCCTCCTCLLACL CT CTCCCTAACCTCTAGCCCTCLAGTTGCACLGTGATCAGCCAAACCAGTTTGCCCAAAALT STREEDSTGCCTGCCTGTCAGGTGCTTTATTACTA VATOARGTCATGCCCTCAGGAAGCCGTGT

> TGS: ATCA - DBS + CACAAGO COTTO BAGGED DOTATAC LATGEC DA DETEGRAS DA S AGA - CDAA - DA 1 111 FECO PEGGAA ENCITTOTE GOCAAGTOTEGED CAGEET GOCAGEET GOCAGE DE GOCOTE GOC BGC - TERCEA TEAAR - DOACE COATECT TEATEGECAT GAGGACCACTOG FIET GOTEGE GOGET GOCAGET GOCAGET GOTEGE GOGET GOTEGE GOCAGET GOTEGE GOTE

2.2334 DEC PGAGOT UCCTMATECCAGGAGOCI EGRACA CTC COTAGGCT CCTAGOCT CCTAGGCAGAT AT SPORCE PARA CARGAGA CCORGOT GOTGAGAGA CARGAGAT GOCI CCTAGAGA CARGAGA CARGAGA

22346 TCATCDCA CA SCREEGOA CACTE DOLAGGET DOTACOCTOCCE COPSATSTOCCEG SAA
CA SRAACTES CELSA DOCE SCREEGOACCETOCE SEGCACETESAG CAAT SCROEGAGES SAE
CA CREEA SCREAAA ROCCETE COAGSCREEGETA CATGGOCCACETES SA SCREAGAGA SOC
AA CA POETE CELEGASAAS ETETED POGOCCAS SECTEGOCCASOCTES CELEGAGAGAGA SECTEA CAAGAGA SECTEA CAAGAGA CELEGAGAGA CELEGAGAGAGA CELEGAGAGAGA CELEGAGAGAGA CELEGAGAGAGAGA CELEGAGAGAGA CELEGAGAGAAAAA

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23445 AGGAAACT BET STEINAAAAAGGAAAAG EGACT DACCAAGGT DACAAGTA GGAAGT GACG CTG: GGGAAACCI BECT LAGGGGAACAAGACCT GGCGGGCAGGCTTGCAGCTCCT DAA CTAAAATACT GAAAATGA GGGGCTTCGATGATG STTATAAT EG FATG GCAGAGCCCCAAL

FIGURE 3, page 20 of 22

THAACTGGAGOUTTGGGADU TAGAAD (TAGGGTOTCACTCUÓTGCTTTT) CACAAGGGAC CATTAGGGCATCA CCCDAGGUCTCG PLAGGCACGAGGGAGGGATCCTGGCTCTCATTGGT CATTAG

GGG SUCTTA SGGGUTCTUGGUTG LICH TITTGAAGAGGGGG PTCAGCUCAGCGAGS DAC DO CCTA FECTG DACCCCACDA AGGTTAGGAAGAGGTC DTETU DTCAGTGG EGCCCCT DE BANG AACAB BCCA FOAGGTUTED STOCACAT EUC FTGGAABAGA FGG FGACA FAATTAAA DE T TTGAABCCC DATATTAAAD DACCTAGABAB NOATC PETATA CETTTAG ECTCTBABAA A T TAGGBBAAB FAABCAATTAAAACANT FOT FTATA FEGUDO ABGTGCAATG DDACCE

AAAAAAAAAAA TIGAA BA PA PET KOTIGA NAA GACCIC NGCIC PIG CAAA CITICA 36366 CAGCIC NA 16 BAGGITAK BIRAAA TIGAA BILINGGA GIIT KAGCIC DODOO DA DA CICITO DA CICICI DODOO DO CICICA GIIT NA 18 FI BIRINGGA DI CICICI PICO DA CICICA TICICA GIITO DO CICICA GIITO DA GIITO PAGTIC PICE GIITA A CACAM BIRINGGA DA GIITO DA GIITO GIITO SIA CAATUU SIO A GGAAT CUIDAA GAAAAA DA SIITI SA GIITA GIITA GIITA GIITA GA

> -SAA DO COOT LITPOCAS EGGAA É COOL BA POAT BOIT SO TIPTOTEC DE STIE BAGAREGAT NAA G BACOT SIE DO DA COOME ETTO E E E E E E E ETITE SAVA ES SAS TE ET SOT CAT SOT HID CO AGGOT SIE BEFA CAAT BIFTAN HAT OF MAISOT DA DIEGOAA DO FOTACOTHO DO SIE E FOAA HO BGOT OF COOP FOOTTAN DOTO DICCAGINAS OF SOGRATIA DE SOCATORA DICACIA CACINA DICAGA A DI DIAA E E INGENE PETTANTANA SATUKES E ETITOT DATO PROGROAS SOT SIE COMA A D

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> SGÒ DE DO TANASTACE SIGGATTACAGOSTE SAGODACE PODO DUGGODIAGISCODA DIGIA STETERA NA SGOTERO DISTIGUIAGENI ROAT DOA SACOISA SEGONGAACHOAAAGENGAA SGOCA SANG PECA SUGAAGIGUIGAGENINGA SEE SAOCA SECTETEGICTOCICA SGOTO A ANACODIANCEOCAGIC DECENI (ACANCAGI SIGGENITAGASCA EGENGAATICAGAGA HA S SCEIGA SCHAFIGONOCOCOGANAGACHIGGAAFGOCACE SAGODACAGAGACOCAGENICA

25529 AGTGCAGAAACTCAAAGTTGAAGGCCAGAAGCTCAGGGAAGGCGGAGGTGAGCTTGAGGAA GTCTCTTGGCTGCCAGGGCCAGAAACCGAACTCCAAGCCTCTCCACAACAGGCGGT\*\*TAG AS PATETABAATEAGAGAGGGGGGGAGA DIATBEAGGGGGGGAGABAKS BAATE DIA ET GAR DIAMAKANAGCAGTGGCAGTGGLAGGTGTCTFGGGTGGACTTGGGATGATER [T,G]

25614 GGC CAGAA DE PAGGGAAGEGAGT DE AG PTGA DIA JTE TE PEGE ET 3.1 JAGGGCA G AAA DEGAA DE DAA BE DE POCA PAA DA BEGGGT GEAGA DE AGAGA E BAGAGGA G GCT BAG DIATECA DE CODERGAGA GA GGGA DEGE DA DAGAGCA DAGAGA DE CAGAGGA DE CAGAGA DE

> OCCATAA DAT DAG UDD DO DAGA SA SEGEGA DAA DIEGOT GA SEITGA FAACA FAATAGA EG DE DOT ETO DIESGAG GEDA EGGEDATEG EDAG DE EGGA GA GA GEAA GOODEAAS DAAG GA GGA FOGGGGG GIT DIAGA GGEGAA GEAAG EGAAA GITGAA GAIT TA TAAGA DOTGINGIT DA GGITGGOO FGGGAA GGETTI GA DEAGTEG DE DE DE DE DAAA GAGET FGAAA GGEGA ETITGICH GOITGITGGIT GAGDAO EG DO DO DOOCITA GEGAD AAACA GUCAAC DOTT EED DOOCATITEG OUTTEDOO

25785 DOA STG DOAD TG DIAMGT GIDTTO DA CTID DOAT BACCDOGGOCT STOT OTGTAT B CAGGOT FOADOO INTOTOG IN STAIDANT SIACACA PTOTA GETGACADOAGCA SONTOT B ATTIDTCAT CTOCOBA FAACA IDAGCIDO DA BAGAG SIGGA (AA CTGCTGAG CTGATA DA F AATAGA FIGODOO IT FOOTIG BAGGO DA FIGGINGAG (ET GAGAGGATGAAGOCTGA GCAGGCAGGATO GGGGGTC FA BAGGO BAA GGAGGAA FITT BAGATCACAGA COTGITG G FOURT

> CAGGTGGCCTGGGAAGGGTTT GACGA STGTC \$ SOCICAAA (AGCTTGGAAGGGATTTTGCT GCTGTGGGTGAGCACTGCCTCCCCCTTA GGSACAACA G (CACCTCTTCTCTCCCCCATTT GCCTTTCCCTTCTGTAGATAT GAAACACAGGCCTTCCTT S CCAGGCCCCTACTTAACCTCC GTGATGGGGAAAGCGGCCGGA GAAAGGGA GTTCTGGCA G (TTCTCCCGAGACCCCCAACACC CCACTGTTGCAAGGTGAGTCATGGCCTGACAC ICTGGCTGTCCCCTACCCCAAGCTTA